

Amendments to the Specification

Please amend the specification as follows.

Please delete paragraph [0029] and replace it with the following amended paragraph [0029]:

[0029] Figure 4 is an image of the structure of HAUSP N-terminal domain. The HAUSP N-terminal TRAF-like domain adopts an eight-stranded antiparallel beta sandwich structure, with strands (beta)1, (beta)5 and (beta)6, and (beta)8 in one sheet and (beta)2, (beta)3, (beta)4, and (beta)7 in the other. The overall structure of the HAUSP TRAF-like domain resembles the TRAF-C domain of the TRAF family of proteins. Figure 4A is a color image that depicts the structure of the HAUSP TRAF-like domain in a ribbon diagram (left portion of the figure) and a surface representation (right portion of the figure). Secondary structural elements in the ribbon diagram and the putative substrate-binding groove in the surface representation are labeled. Figure 4B is alignment of the sequences (HAUSP = SEQ ID NO. 1; TRAF1 = SEQ ID NO. 2; TRAF 2 = SEQ ID NO. 3; TRAF 3 SEQ ID NO. 4, TRAF 4 = SEQ ID NO. 5; TRAF 5 = SEQ ID NO. 6; and TRAF 6 = SEQ ID NO. 7) of HAUSP TRAF-like domain with other TRAF family members. Conserved residues are highlighted in yellow. HAUSP residues that interact with p53 through hydrogen bonds and van der Waals contacts are identified by green triangles and green squares, respectively. HAUSP residues that interact with MDM2 through hydrogen bonds and van der Waals contacts are indicated by red triangles and red squares, respectively. Conserved residues that are involved in binding to peptides in other TRAF family proteins but not in HAUSP are colored red and highlighted in purple. The ribbon and cylinder diagram above the sequences indicates secondary structures in HAUSP protein.

Following the last paragraph of the specification, before the claims, please insert the paper copy of the Sequence Listing attached.